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 NEWS  1           Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2  Jan 25   BLAST(R) searching in REGISTRY available in STN on the Web
 NEWS  3  Jan 29   FSTA has been reloaded and moves to weekly updates
 NEWS  4  Feb 01   DKILIT now produced by FIZ Karlsruhe and has a new update
                   frequency
 NEWS  5  Feb 19   Access via Tymnet and SprintNet Eliminated Effective 3/31/02
 NEWS  6  Mar 08   Gene Names now available in BIOSIS
 NEWS  7  Mar 22   TOXLIT no longer available
 NEWS  8  Mar 22   TRCTHERMO no longer available
 NEWS  9  Mar 28   US Provisional Priorities searched with P in CA/CAplus
                   and USPATFULL
 NEWS 10  Mar 28   LIPINSKI/CALC added for property searching in REGISTRY
 NEWS 11  Apr 02   PAPERCHEM no longer available on STN.  Use PAPERCHEM2 instead.
 NEWS 12  Apr 08   "Ask CAS" for self-help around the clock
 NEWS 13  Apr 09   BEILSTEIN: Reload and Implementation of a New Subject Area
 NEWS 14  Apr 09   ZDB will be removed from STN
 NEWS 15  Apr 19   US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
 NEWS 16  Apr 22   Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
 NEWS 17  Apr 22   BIOSIS Gene Names now available in TOXCENTER
 NEWS 18  Apr 22   Federal Research in Progress (FEDRIP) now available

 NEWS EXPRESS  February 1 CURRENT WINDOWS VERSION IS V6.0d,
               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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                                                       ENTRY    SESSION
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=> s histone deacetylase
L1 2662 HISTONE DEACETYLASE

=> s l1 and transcription
L2 1411 L1 AND TRANSCRIPTION

=> s l2 and (regulat? or repress or control)
L3 1089 L2 AND (REGULAT? OR REPRESS OR CONTROL)

=> s l3 and express?
L4 632 L3 AND EXPRESS?

=> s l3 and transgenic
L5 26 L3 AND TRANSGENIC

=> dup rem l5
PROCESSING COMPLETED FOR L5
L6 20 DUP REM L5 (6 DUPLICATES REMOVED)

=> d 1-10 ti

L6 ANSWER 1 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI Deregulation of polyamine biosynthesis alters intrinsic histone acetyltransferase and deacetylase activities in murine skin and tumors

L6 ANSWER 2 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI Methods and compositions relating to **histone deacetylase** 4 and 5 **regulation** of cardiac gene expression

L6 ANSWER 3 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI **Transgenic** plants expressing **histone deacetylase** genes for use in **control** of plant development

L6 ANSWER 4 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 1
TI Repressor element silencing **transcription** factor/neuron-restrictive silencing factor (REST/NRSF) can act as an enhancer as well as a repressor of corticotropin-releasing hormone gene **transcription**

L6 ANSWER 5 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI Evidence for epigenetic mechanisms that silence both basal and immune-stimulated **transcription** of the IL-8 gene

L6 ANSWER 6 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 2
TI Intergenic **transcription** in the human .beta.-globin gene cluster

L6 ANSWER 7 OF 20 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Gene targeting reveals a crucial role for MTG8 in the gut.

L6 ANSWER 8 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI **Histone deacetylase** inhibitors induce remission in **transgenic** models of therapy-resistant acute promyelocytic

leukemia

L6 ANSWER 9 OF 20 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI The IL-7 receptor controls the accessibility of the TCRgamma locus by Stat5 and histone acetylation.

L6 ANSWER 10 OF 20 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Igf2/H19 imprinting **control** region (ICR): An insulator or a position-dependent silencer.

=> d 3 ab

L6 ANSWER 3 OF 20 CAPLUS COPYRIGHT 2002 ACS
AB Posttranslational modification of histones, in particular acetylation and deacetylation are involved in the **regulation** of gene expression. Histone deacetylases remove acetyl groups from histone proteins. The present invention is directed to a method of **regulating** gene expression in a **transgenic** plant comprising, introducing into a plant a first chimeric nucleotide sequence comprising a first **regulatory** element in operative assocn. with a gene of interest, and an upstream activating sequence, and a second chimeric nucleotide sequence comprising a second **regulatory** element in operative assocn. with a nucleotide sequence encoding **histone deacetylase** and a nucleotide sequence encoding a DNA binding protein, and growing the **transgenic** plant. Furthermore, a method for **regulating** gene expression of an endogenous gene of interest, or modifying a developmental, physiol. or biochem. pathway in a plant is provided comprising introducing into a plant a chimeric nucleotide sequence comprising a **regulatory** element in operative assocn. with a nucleotide sequence encoding **histone deacetylase** fused with a nucleotide sequence encoding a DNA binding protein capable of interacting with an endogenous controlling sequence, for example an upstream activating sequence, and growing the **transgenic** plant. This invention also relates to novel **histone deacetylase** obtained from plants, to novel chimeric construct comprising these, or other **histone deacetylase**, and to **transgenic** plants, plant cells, or seeds comprising these chimeric constructs.

=> d 3 pi

L6 ANSWER 3 OF 20 CAPLUS COPYRIGHT 2002 ACS

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI EP 1094112	A2	20010425	EP 2000-307375	20000829

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

=> d 4 ab

L6 ANSWER 4 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 1
AB The repressor element-1/neuron-restrictive silencing element (RE-1/NRSE) mediates transcriptional repression by the repressor element silencing **transcription** factor/neuron-restrictive silencing factor (REST/NRSF) in many neuron-specific genes. REST/NRSF is expressed most highly in non-neural tissues, where it is thought to **repress** gene **transcription**, but is also found in developing neurons and at low levels in the brain. Its null mutation in vivo results in embryonic lethality in mice. While the RE-1/NRSE-mediated repressive influence of REST/NRSF is well established, results in **transgenic** studies have suggested that the action of the system is more complex.

Here, the authors report that **transcription** of the corticotropin releasing hormone (CRH) gene is **regulated** by REST/NRSF, in part through the RE-1/NRSE. Expression of transfected Crh-luciferase constructs was down-**regulated** by REST/NRSF in a RE-1/NRSE-dependent fashion in both muscle-derived L6 and REST/NRSF co-transfected neuronal PC12 cells. Treatment of L6 cells with trichostatin A revealed that REST/NRSF repression depends, in part, on **histone deacetylase** activity in these cells. In another neuronal cell line, NG108, REST/NRSF also repressed expression from constructs contg. an intact RE-1/NRSE. However, unexpectedly, REST/NRSF up-**regulated** expression levels of constructs lacking an intact RE-1/NRSE. These results suggest that REST/NRSF can act as both a repressor of Crh **transcription**, via the Crh RE-1/NRSE, and an enhancer of Crh **transcription**, via a mechanism independent of the Crh RE-1/NRSE.

=> d 3 au

L6 ANSWER 3 OF 20 CAPLUS COPYRIGHT 2002 ACS
IN Wu, Keqiang; Miki, Brian L. A.; Tian, Lining; Brown, Daniel C. W.

=> d 7 ab

L6 ANSWER 7 OF 20 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AB The MTG8 (ETO) locus is involved in a reciprocal exchange with runx1 in the t(8;21) of acute myeloid leukemia. It is a member of a small gene family encoding transcriptional **regulators** that interact with corepressors and **histone deacetylase**. However, the physiologic cellular processes controlled by MTG8 are not known. In order to gain an insight into the latter, we have generated mutant mice with an insertional inactivation at the locus, which disrupts **transcription** of exon 2. The postnatal viability of homozygous mutants was greatly reduced. In approximately 25% the midgut was missing, whereas practically all pups surviving past the first 2 days showed severe growth impairment, which was likely due to a gross disruption of the gut architecture. The latter phenotype could be traced back to late embryonic development. No difference in gut cell differentiation or proliferation was found compared to wild-type littermates. Levels of factors known to be involved in gut morphogenesis were also unchanged. MTG8 is expressed in the outermost layers of the developing gut from at least E9.5. Thus, MTG8 plays a novel, essential role in the gastrointestinal system.

=> d 11-20 ti

L6 ANSWER 11 OF 20 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Role for the nuclear protein kinase HIPK2 in corepressor activity of Groucho during development.

L6 ANSWER 12 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 3
TI Blocking histone deacetylation in Arabidopsis induces pleiotropic effects on plant gene **regulation** and development

L6 ANSWER 13 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI An Ikaros-containing chromatin-remodeling complex in adult-type erythroid cells

L6 ANSWER 14 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI Atrophin-1, the dentato-rubral and pallido-luysian atrophy gene product, interacts with ETO/MTG8 in the nuclear matrix and represses **transcription**

L6 ANSWER 15 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 4
TI Functional analysis of a RPD3 **histone deacetylase** homologue in Arabidopsis thaliana

L6 ANSWER 16 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 5
TI DNA methylation and histone deacetylation in the **control** of gene expression: basic biochemistry to human development and disease

L6 ANSWER 17 OF 20 AGRICOLA DUPLICATE 6
TI Functional analysis of HD2 **histone deacetylase** homologues in Arabidopsis thaliana.

L6 ANSWER 18 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI Functional analysis of HD2 **histone deacetylase** homologs in Arabidopsis thaliana

L6 ANSWER 19 OF 20 AGRICOLA
TI A screen for mutations that prevent lethality caused by expression of activated sevenless and Ras1 in the Drosophila embryo.

L6 ANSWER 20 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI Distinct interactions of PML-RAR.alpha. and PLZF-RAR.alpha. with co-repressors determine differential responses to RA in APL

=> d 12 ab

L6 ANSWER 12 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 3
AB Histone acetylation and deacetylation play essential roles in eukaryotic gene **regulation**. Reversible modifications of core histones are catalyzed by two intrinsic enzymes, histone acetyltransferase and **histone deacetylase** (HD). In general, histone deacetylation is related to transcriptional gene silencing, whereas acetylation correlates with gene activation. **Transgenic** plants were produced expressing the antisense Arabidopsis HD (AtHD1) gene. AtHD1 is a homolog of human HD1 and RPD3 global transcriptional **regulator** in yeast. Expression of the antisense AtHD1 caused dramatic redn. in endogenous AtHD1 **transcription**, resulting in accumulation of acetylated histones, notably tetraacetylated H4. Redn. in AtHD1 expression and AtHD1 prodn. and changes in acetylation profiles were assocd. with various developmental abnormalities, including early senescence, ectopic expression of silenced genes, suppression of apical dominance, homeotic changes, heterochromic shift toward juvenility, flower defects, and male and female sterility. Some of the phenotypes could be attributed to ectopic expression of tissue-specific genes (e.g., SUPERMAN) in vegetative tissues. No changes in genomic DNA methylation were detected in the **transgenic** plants. These results suggest that AtHD1 is a global **regulator**, which controls gene expression during development through DNA-sequence independent or epigenetic mechanisms in plants. In addn. to DNA methylation, histone modifications may be involved in a general **regulatory** mechanism responsible for plant plasticity and variation in nature.

=> d 12 so

L6 ANSWER 12 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 3
SO Proceedings of the National Academy of Sciences of the United States of America (2001), 98(1), 200-205
CODEN: PNASA6; ISSN: 0027-8424

=> d 15 ab

L6 ANSWER 15 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 4
AB Histone acetylation is modulated through the action of histone acetyltransferase and deacetylase, which play key roles in the **regulation** of eukaryotic gene expression. We have screened the expressed sequence tag database with the yeast **histone deacetylase** RPD3 sequence and identified two Arabidopsis homologues, AtRPD3A and AtRPD3B. The deduced amino acid sequences of AtRPD3A and AtRPD3B show high overall homol. (55% identity) to each other. AtRPD3A encodes a putative protein of 502 amino acids with 49% identity to the yeast RPD3. AtRPD3B encodes a putative protein of 471 amino acids and shares 55% amino acid identity with the yeast RPD3. Northern anal. indicated that AtRPD3A was highly expressed in the leaves, stems, flowers and young siliques of Arabidopsis plants, whereas the AtRPD3B transcript was not detected in these organs. An AtRPD3A fusion protein repressed **transcription** when directed to a promoter driving a reporter gene, indicating a role for AtRPD3A protein in gene repression. Arabidopsis plants were transformed with a gene construct comprising a truncated AtRPD3A cDNA in the antisense orientation driven by a strong constitutive promoter, -394tCUP. Antisense expression of AtRPD3A resulted in decreased endogenous AtRPD3A transcript and delayed flowering in **transgenic** Arabidopsis plants, suggesting that the transition from the vegetative to reproductive phase of development could be affected by histone acetylation. Our study demonstrates the important role of histone deacetylases in plant growth and development.

=> d 15 so

L6 ANSWER 15 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 4
SO Plant Molecular Biology (2000), 44(2), 167-176
CODEN: PMBIDB; ISSN: 0167-4412

=> d 16 ab

L6 ANSWER 16 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 5
AB A review with 125 refs. DNA methylation is a major determinant in the epigenetic silencing of genes. The mechanisms underlying the targeting of DNA methylation and the subsequent repression of **transcription** are relevant to human development and disease, as well as for attempts at somatic gene therapy. The success of **transgenic** technologies in plants and animals is also compromised by DNA methylation-dependent silencing pathways. Recent biochem. expts. provide a mechanistic foundation for understanding the influence of DNA methylation on **transcription**. The DNA methyltransferase Dnmt1, and several methyl-CpG binding proteins, MeCP2, MBD2, and MBD3, all assoc. with **histone deacetylase**. These observations firmly connect DNA methylation with chromatin modifications. They also provide new pathways for the potential targeting of DNA methylation to repressive chromatin as well as the assembly of repressive chromatin on methylated DNA. Here we discuss the implications of the methylation-acetylation connection for human cancers and the developmental syndromes Fragile X and Rett, which involve a mistargeting of DNA methylation-dependent repression.

=> d 16 so

L6 ANSWER 16 OF 20 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 5
SO Gene Expression (2000), 9(1/2), 63-75
CODEN: GEEXEJ; ISSN: 1052-2166

=> d 17 ab

L6 ANSWER 17 OF 20 AGRICOLA DUPLICATE 6
AB Post-translational modification of histones, in particular acetylation, is an important mechanism in the **regulation** of eukaryotic gene expression. Histone deacetylases are enzymes that remove acetyl groups from the core histones and play a key role in the repression of **transcription**. HD2 is a maize **histone deacetylase**, which shows no sequence homology to the histone deacetylases identified from other eukaryotes. We have identified two putative HD2-like **histone deacetylase** cDNA clones, AtHD2A and AtHD2B, from Arabidopsis thaliana by screening the expressed sequence tag database. AtHD2A and AtHD2B encode putative proteins of 246 and 305 amino acids, and share 44% and 46% amino acid identity to the maize HD2, respectively. Northern blot analysis indicated that AtHD2A was highly expressed in flowers and young siliques of Arabidopsis plants, whereas AtHD2B was widely expressed in stems, leaves, flowers and young siliques. AtHD2A repressed **transcription** when directed to a promoter containing GAL4-binding sites as a GAL4 fusion protein. Deletion of the extended acidic domain or the domain containing predicted catalytic residues of AtHD2A resulted in the loss of gene repression activity, revealing the importance of both domains to AtHD2A function. Arabidopsis plants were transformed with a gene construct comprising an AtHD2A cDNA in the antisense orientation driven by a strong constitutive promoter, -394tCUP. Silencing of AtHD2A expression resulted in aborted seed development in **transgenic** Arabidopsis plants, suggesting that the AtHD2A gene product was important in the reproductive development of Arabidopsis thaliana.

=> d 17 so

L6 ANSWER 17 OF 20 AGRICOLA DUPLICATE 6
SO The Plant journal : for cell and molecular biology, Apr 2000. Vol. 22, No. 1. p. 19-27
Publisher: Oxford : Blackwell Sciences Ltd.
ISSN: 0960-7412

=> s atrpd3a
L7 3 ATRPD3A

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8 2 DUP REM L7 (1 DUPLICATE REMOVED)

=> d 1-2 ti

L8 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2002 ACS
TI Transgenic plants expressing histone deacetylase genes for use in control of plant development

L8 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 1
TI Functional analysis of a RPD3 histone deacetylase homologue in Arabidopsis thaliana

=> s atrpd3b
L9 2 ATRPD3B

=> dup rem l9
PROCESSING COMPLETED FOR L9
L10 1 DUP REM L9 (1 DUPLICATE REMOVED)

=> d ti

L10 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 1
TI Functional analysis of a RPD3 histone deacetylase homologue in Arabidopsis thaliana

=> s athd2a or athd2b
L11 4 ATHD2A OR ATHD2B

=> dup rem l11
PROCESSING COMPLETED FOR L11
L12 3 DUP REM L11 (1 DUPLICATE REMOVED)

=> d 1-3 ti

L12 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2002 ACS
TI Transgenic plants expressing histone deacetylase genes for use in control of plant development

L12 ANSWER 2 OF 3 AGRICOLA DUPLICATE 1
TI Functional analysis of HD2 histone deacetylase homologues in Arabidopsis thaliana.

L12 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2002 ACS
TI Functional analysis of HD2 histone deacetylase homologs in Arabidopsis thaliana

=> s l1 and mammalian
L13 248 L1 AND MAMMALIAN

=> s l13 and repression
L14 120 L13 AND REPRESSION

=> s l14 and transgenic
L15 0 L14 AND TRANSGENIC

=> s l14 and (transform? or transdu?)_
MISSING OPERATOR TRANSDU?)_
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l14 and (transform? or transdu?)
L16 13 L14 AND (TRANSFORM? OR TRANSDU?)

=> dup rem l16
PROCESSING COMPLETED FOR L16
L17 8 DUP REM L16 (5 DUPLICATES REMOVED)

=> d 1-8 ti

L17 ANSWER 1 OF 8 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 1
TI A conserved .alpha.-helical motif mediates the interaction of Sp1-like transcriptional repressors with the corepressor mSin3A

L17 ANSWER 2 OF 8 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 2
TI Pf1, a novel PHD zinc finger protein that links the TLE corepressor to the mSin3A-**histone deacetylase** complex

L17 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2002 ACS
TI Activation of the myocyte enhancer factor-2 transcription factor by calcium/calmodulin-dependent protein kinase-stimulated binding of 14-3-3 to **histone deacetylase** 5

L17 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 3
TI Expression of Transcriptional Repressor Proteins mSin3A and 3B during Aging and Replicative Senescence

L17 ANSWER 5 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Reprogramming of gene expression during preimplantation development.

L17 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 4
TI The three members of the pocket proteins family share the ability to repress E2F activity through recruitment of a **histone deacetylase**

L17 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 5
TI A **histone deacetylase** corepressor complex regulates the Notch signal **transduction** pathway

L17 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2002 ACS
TI Thyroid hormone and gut differentiation: molecular mechanisms of action

=> d 7 ab

L17 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 5
AB The Delta-Notch signal **transduction** pathway has widespread roles in animal development in which it appears to control cell fate. CBF1/RBP-J.kappa., the **mammalian** homolog of Drosophila Suppressor of Hairless [su(H)], switches from a transcriptional repressor to an activator upon Notch activation. The mechanism whereby Notch regulates this switch is not clear. In this report we show that prior to induction CBF1/RBP-J.kappa. interacts with a corepressor complex contg. SMRT (silencing mediator of retinoid and thyroid hormone receptors) and the **histone deacetylase** HDAC-1. This complex binds via the CBF1 **repression** domain, and mutants defective in **repression** fail to interact with the complex. Activation by Notch disrupts the formation of the repressor complex, thus establishing a mol. basis for the Notch switch. Finally, ESR-1, a Xenopus gene activated by Notch and X-Su(H), is induced in animal caps treated with TSA, an inhibitor of HDAC-1. The functional role for the SMRT/HDAC1 complex in CBF1/RBP-J.kappa. regulation reveals a novel genetic switch in which extracellular ligands control the status of crit. nuclear cofactor complexes.

=> s l1 and gal4
L18 60 L1 AND GAL4

=> s l18 and transgenic
L19 5 L18 AND TRANSGENIC

=> dup rem l19
PROCESSING COMPLETED FOR L19
L20 4 DUP REM L19 (1 DUPLICATE REMOVED)

=> d 1-4 ti

L20 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2002 ACS
TI Methods and compositions relating to **histone deacetylase** 4 and 5 regulation of cardiac gene expression

L20 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2002 ACS
TI **Transgenic** plants expressing **histone deacetylase** genes for use in control of plant development

L20 ANSWER 3 OF 4 AGRICOLA DUPLICATE 1

TI Functional analysis of HD2 **histone deacetylase** homologues in Arabidopsis thaliana.

L20 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2002 ACS
TI Functional analysis of HD2 **histone deacetylase** homologs in Arabidopsis thaliana

=> d so

L20 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2002 ACS
SO PCT Int. Appl., 126 pp.
CODEN: PIXXD2

=> d pi

L20 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2002 ACS

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001014581	A2	20010301	WO 2000-US22958	20000821
WO 2001014581	A3	20010920		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

=> d ab

L20 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2002 ACS
AB The invention relates to cardiac hypertrophy. More particularly, the invention defines the mol. events linking calcium stimulation to cardiac hypertrophy. More specifically, the invention shows that Ca2+ stimulation of the hypertrophic response is mediated through an **histone deacetylase** (HDAC) 4 and 5 interaction with myocyte enhancer factor 2 (MEF2), and that phosphorylation of HDACs results in loss of HDAC-mediated repression of MEF2 hypertrophic action. Thus, the invention provides methods and compns. of treating cardiac hypertrophy, as well as methods and compns. for identifying subjects at risk for cardiac hypertrophy. Further provided are methods for the detection of compds. having therapeutic activity toward cardiac hypertrophy.